

GenCore version 4.5  
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## OM protein - protein search, using sw model.

Run on: June 24, 2002, 20:51:21 ; Search time 11.84 Seconds  
(without alignments)

212.565 Million cell updates/sec

Title: Perfect score: US-09-664-326-23

Sequence: 1 LTYDCTESQNLCLCEGSN..... PKPQSHNDGDFEEFPEEYIQL 65

Scoring table: BLASTng62 Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot:40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARES

\* Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	350	97.8	65	1	ITHL_HIRME	P0150	hirudo medi
2	353	95.9	65	1	ITHE_HIRME	P28506	hirudo medi
3	352	95.7	65	1	ITHC_HIRME	P28511	hirudo medi
4	350	95.1	65	1	ITHD_HIRME	P28503	hirudo medi
5	348	94.6	65	1	ITHI_HIRME	P28504	hirudo medi
6	348	94.6	65	1	ITHE_HIRME	P28509	hirudo medi
7	346	94.0	65	1	ITHG_HIRME	P28508	hirudo medi
8	345	93.8	65	1	ITHJ_HIRME	P28510	hirudo medi
9	345	93.8	65	1	ITHE_HIRME	P28505	hirudo medi
10	343	93.2	65	1	ITHE_HIRME	P09945	hirudo medi
11	333	90.5	72	1	ITH2_HIRME	P09944	hirudo medi
12	315	85.6	66	1	ITHA_HIRME	P28501	hirudo medi
13	293	79.6	65	1	ITHY_HIRMA	P18192	hirudinaria
14	249	67.7	63	1	ITH6_HIRMA	P28512	hirudinaria
15	215	58.4	63	1	ITHP_HIRMA	P26531	hirudinaria
16	173	47.0	62	1	ITHB_HIRME	P28502	hirudo medi
17	90	24.5	17	1	VATA_YEAST	P17255	saccharomyces
18	68	18.6	1071	1	YDX_RHISN	P5512	rhizobium s
19	68	18.5	192	1	OS28_PLAGA	Q05339	plasmidium
20	67	18.2	22	1	IBP2_SHEEP	Q92332	homo sapien
21	66.5	18.1	810	1	NELL_HUMAN	P57999	oryctolagous
22	66	17.9	2282	1	ZAN_RABIT	088799	mus musculus
23	66	17.9	5376	1	ZAN_MOUSE	09Y193	homo sapien
24	65	17.8	2700	1	ZAN_HUMAN	015165	homo sapien
25	65	17.7	317	1	IBP2_SHEEP	Q29400	oryz aries
26	64	17.4	318	1	GSHB_VTBCH	Q9kp7	vibrio cholerae
27	63.5	17.3	474	1	VSM5_TRYBB	P26333	trypanosoma
28	63.5	17.3	755	1	COMP_RAT	P3544	rattus norvegicus
29	63.5	17.3	2703	1	NOTC_DRONE	P07207	drosophila
30	63.5	17.3	80	1	AEP4_RAPSA	O24331	raphanus sativus
31	63	17.1	385	1	GUNF_FUSOX	P46239	fusarium oxysporum
32	63	17.1	513	1	AVR2_HUMAN	P27037	homo sapien

ALIGNMENTS

RESULT	1	ITHL_HIRME	STANDARD:	PRT:	65 AA.
ID	ITHL_HIRME	ID	ITHL_HIRME		
AC	P0150;	AC	P0150;		
DT	21-JUL-1986	DT	21-JUL-1986	( Rel. 01, Created)	
	( Rel. 01, last sequence update)		( Rel. 01, last sequence update)		
DE	Hirudin variant-1 (Leprudin).	DE	Hirudin variant-1 (Leprudin).		
OS	Hirudo medicinalis (Medicinal leech).	OS	Hirudo medicinalis (Medicinal leech).		
OC	Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;	OC	Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;		
OX	NCBI_TaxID=6421;	OX	NCBI_TaxID=6421;		
RN	[1]	RN	[1]		
RP	SEQUENCE.	RP	SEQUENCE.		
RA	Petersen T.E., Roberts H.R., Sottrup-Jensen L., Magnusson S.,	RA	Dodd J., Mueller H.-P., Seemueller U., Chang J.-Y.,		
RA	Bagdy D.,	RA	Dodd J., Mueller H.-P., Seemueller U., Chang J.-Y.,		
RL	(In Peeters H. (eds.);	RL	"The complete amino acid sequence of hirudin, a thrombin specific		
RL	Proteides of the biological fluids, Proc. 23th colloquium, pp.145-149,	RL	inhibitor. Application of colour carboxymethylation.",		
RL	Peramon Press, New York (1976).	RL	FEBS Lett. 165:180-183(1984).		
RP	[3]	RP	[3]		
STRUCTURE BY NMR:		STRUCTURE BY NMR:			
RA	MEDLINE=89274194; PubMed=2567183;	RA	Folkers P.J.M., Clore G.M., Driscoll P.C., Dodd J., Koehler S.,		
RA	Gronenborn A.M.;	RA	Gronenborn A.M.;		
RA	"Solution structure of recombinant hirudin and the Lys<47-->Glu	RA	"Solution structure of recombinant hirudin and the Lys<47-->Glu		
RT	mutant: a nuclear magnetic resonance and hydrid distance	RT	mutant: a nuclear magnetic resonance and hydrid distance		
RT	geometry-dynamical simulated annealing study.";	RT	geometry-dynamical simulated annealing study.";		
RL	Biochemistry 28:2601-2617(1989).	RL	Biochemistry 28:2601-2617(1989).		
RN	[4]	RN	[4]		
RP	STRUCTURE BY NMR OF 1-51.	RP	STRUCTURE BY NMR OF 1-51.		
RA	MEDLINE=93116062; PubMed=1333515;	RA	Szyperski T., Guentert P., Stone S. R., Wuetrich K.;		
RA	"Nuclear magnetic resonance solution structure of hirudin(1-51) and	RA	"Nuclear magnetic resonance solution structure of hirudin(1-51) and		
RT	comparison with corresponding three-dimensional structures determined	RT	comparison with corresponding three-dimensional structures determined		
RT	using the complete 65-residue hirudin polypeptide chain.";	RT	using the complete 65-residue hirudin polypeptide chain.";		
RL	J. Mol. Biol. 228:1193-1205(1992).	RL	J. Mol. Biol. 228:1193-1205(1992).		
CC	-I - FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE	CC	-I - FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE		
CC	INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-	CC	INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-		
CC	THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.	CC	THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.		
CC	-I - PHARMACEUTICAL: Available under the name Refludan (Hoechst Marion	CC	-I - PHARMACEUTICAL: Available under the name Refludan (Hoechst Marion		
CC	Roussel). Used to treat heparin-induced thrombocytopenia (HIT).	CC	Roussel). Used to treat heparin-induced thrombocytopenia (HIT).		
CC	-I - SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.	CC	-I - SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.		
CC	-I - DATABASE: NAME=Refludan; NOTE=Clinical information on Refludan;	CC	-I - DATABASE: NAME=Refludan; NOTE=Clinical information on Refludan;		
CC	WWW="http://www.refludan.com/".	CC	WWW="http://www.refludan.com/".		
DR	PIR; A01289; HULX9.	DR	PIR; A01289; HULX9.		
DR	PDB; 2HIR; 15-JAN-90.	DR	PDB; 2HIR; 15-JAN-90.		
DR	PDB; 4HIR; 15-JAN-90.	DR	PDB; 4HIR; 15-JAN-90.		
DR	PDB; 5HTR; 15-JAN-90.	DR	PDB; 5HTR; 15-JAN-90.		
DR	PDB; 6HIR; 15-JAN-90.	DR	PDB; 6HIR; 15-JAN-90.		
PDB	1HIC; 31-JAN-94.	PDB	1HIC; 31-JAN-94.		

Query Match		95.9%	Score	353;	DB	1;	Length	65;	
		Best Local Similarity	93.8%	Pred.	No.	9.1e-32;	Indels	0;	Gaps
		Matches	61;	Conservative		4;	Mismatches	0;	
DR	PDB; 1IHA; 20-DEC-94.								
DR	InterPro; IPR000429; Hirudin.								
DR	Pfam; PF00713; Hirudin; 1.								
DR	PRINTS; PR0077; HIRUDIN.								
DR	PRODOM; PD004216; Hirudin.								
KW	Serine protease inhibitor; Sulfation; Multigene family; Pharmaceutical; 3D-structure.								
FT	DISULFID	6	14						
FT	DISULFID	16	28						
FT	DISULFID	22	39						
FT	MOD_RES	63	63	SULFATION.					
FT	STRAND	5	5						
FT	STRAND	9	10						
FT	STRAND	11	12						
FT	STRAND	15	17						
FT	TURN	18	19						
FT	STRAND	20	21						
FT	TURN	24	25						
FT	STRAND	26	29						
FT	STRAND	38	41						
FT	STRAND	45	46						
SQ	SEQUENCE	65 AA;	6970 MW;	9085A5876E3DE9FF CRC64;					
RESULT	2								
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ID	ITRF_HIRME								
STANDARD;									
PRT;		65 AA.							
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Db	1	VVYDCTESTSGQNLCILCCEGSNVCGQGNKCLIGSDGEKNQCVTGECTPKPQSHNDGDFEEIP	60						
QY	61	EEVYLO	65						
Db	61	EEVYLO	65						
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ID	ITRF_HIRME								
STANDARD;									
PRT;		65 AA.							
Matches	63;	Conservative	1;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	EEVYLO	65						
Db	1	VVYDCTESTSGQNLCILCCEGSNVCGQGNKCLIGSDGEKNQCVTGECTPKPQSHNDGDFEEIP	60						
QY	61	EEVYLO	65						
RESULT	2								
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ID	ITRF_HIRME								
STANDARD;									
PRT;		65 AA.							
Matches	63;	Conservative	1;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	LTYNDCTESGQNLCILCCEGSNVCGQGNKCLIGSDGEKNQCVTGECTPKPQSHNDGDFEEIP	60						
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QY	61	EEVYLO	65						
Db	61	EEVYLO	65						
RESULT	2								
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QY	61	EEVYLO	65						
Db	61	EEVYLO	65						
RESULT	2								
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ID	ITRF_HIRME								
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PRT;		65 AA.							
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QY	1	LTYNDCTESGQNLCILCCEGSNVCGQGNKCLIGSDGEKNQCVTGECTPKPQSHNDGDFEEIP	60						
Db	1	VVYDCTESTSGQNLCILCCEGSNVCGQGNKCLIGSDGEKNQCVTGECTPKPQSHNDGDFEEIP	60						
QY	61	EEVYLO	65						
Db	61	EEVYLO	65						
RESULT	2								
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ID	ITRF_HIRME								
STANDARD;									
PRT;		65 AA.							
Matches	63;	Conservative	1;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	LTYNDCTESGQNLCILCCEGSNVCGQGNKCLIGSDGEKNQCVTGECTPKPQSHNDGDFEEIP	60						
Db	1	VVYDCTESTSGQNLCILCCEGSNVCGQGNKCLIGSDGEKNQCVTGECTPKPQSHNDGDFEEIP	60						
QY	61	EEVYLO	65						
Db	61	EEVYLO	65						
RESULT	2								
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ID	ITRF_HIRME								
STANDARD;									
PRT;		65 AA.							
Matches	63;	Conservative	1;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	LTYNDCTESGQNLCILCCEGSNVCGQGNKCLIGSDGEKNQCVTGECTPKPQSHNDGDFEEIP	60						
Db	1	VVYDCTESTSGQNLCILCCEGSNVCGQGNKCLIGSDGEKNQCVTGECTPKPQSHNDGDFEEIP	60						
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Db	61	EEVYLO	65						
RESULT	2								
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PRT;		65 AA.							
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Db	61	EEVYLO	65						
RESULT	2								
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ID	ITRF_HIRME								
STANDARD;									
PRT;		65 AA.							
Matches	63;	Conservative	1;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	LTYNDCTESGQNLCILCCEGSNVCGQGNKCLIGSDGEKNQCVTGECTPKPQSHNDGDFEEIP	60						
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Db	61	EEVYLO	65						
RESULT	2								
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ID	ITRF_HIRME								
STANDARD;									
PRT;		65 AA.							
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Db	61	EEVYLO	65						
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ID	ITRF_HIRME								
STANDARD;									
PRT;		65 AA.							
Matches	63;	Conservative	1;	Mismatches	1;	Indels	0;	Gaps	0;
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Db	61	EEVYLO	65						
RESULT	2								
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ID	ITRF_HIRME								
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RESULT	2								
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STANDARD;									
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Db	61	EEVYLO	65						
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QY	61	EEVYLO	65						
Db	61	EEVYLO	65						
RESULT	2								
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STANDARD;									
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Db	1	VVYDCTESTSGQNLCILCCEGSNVCGQGNKCLIGSDGEKNQCVTGECTPKPQSHNDGDFEEIP	60						
QY	61	EEVYLO	65						
Db	61	EEVYLO	65						
RESULT	2								
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ID	ITRF_HIRME								
STANDARD;									
PRT;		65 AA.							
Matches	63;	Conservative	1;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	LTYNDCTESGQNLCILCCEGSNVCGQGNKCLIGSDGEKNQCVTG							



OX NCBI\_TaxID=6421;  
 RN [1]  
 RP SEQUENCE; No. 6.6e-31; Pred. No. 6.6e-31;  
 RX MEDLINE=90005945; PubMed=2792365;  
 RA Scharf M., Engels J., Tripler D.;  
 RT "Primary structures of new 'iso-hirudins'.";  
 RL FIBS Lett. 255:105-110(1989)  
 -!- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE  
 INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-  
 THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.  
 CC -!- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.  
 DR HSSP; P01050; IHAG.  
 DR Interpro; IPR000429; Hirudin.  
 DR Pfam; PF00713; Hirudin; 1.  
 DR PRINTS; PR00777; HIRUDIN.  
 DR Prod04216; Hirudin; 1.  
 KW Serine protease inhibitor; Sulfation; Multigene family.  
 FT DISULFID 6 14  
 FT DISULFID 16 28  
 FT MOD\_RES 22 39  
 FT SEQUENCE 65 AA; 6973 MW; CA8BED72B6449E4 CRC64;

Query Match 93.8%; Score 345; DB 1; Length 65;  
 Best Local Similarity 92.3%; Pred. No. 6.6e-31;  
 Matches 60; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 DR P28507;  
 AC P28507;  
 QY 1 LTYDCTESQNLCLCEGSNVCGQGNKCIQSGDGERNQCVTGECPKQPSHNDGFEETP 60  
 DB 1 VVYDCTESQNLCLCEGSNVCGEGNKCILGSNGERNQCVTGECPKQPSHNDGFEETP 60  
 DR 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-DEC-1992 (Rel. 24, Last annotation update)  
 DE Hirudin IIIB.  
 OS Hirudo medicinalis (Medicinal leech);  
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
 OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.  
 OX NCBI\_TaxID=6421;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90005945; PubMed=2792365;  
 RA Scharf M., Engels J., Tripler D.;  
 RT "Primary structures of new 'iso-hirudins'.";  
 RL FIBS Lett. 255:105-110(1989)  
 -!- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE  
 INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-  
 THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.  
 CC -!- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.  
 DR PIR; S05677; S05677.  
 DR Interpro; P01050; IHAG.  
 DR Pfam; PF00713; Hirudin; 1.  
 DR PRINTS; PR00777; HIRUDIN.  
 DR Prod04216; Hirudin; 1.  
 KW Serine protease inhibitor; Sulfation; Multigene family.  
 FT DISULFID 6 14  
 FT DISULFID 16 28  
 FT DISULFID 22 39  
 FT MOD\_RES 63 63  
 FT SEQUENCE 65 AA; 7026 MW; 1E902A81AE3DE9FC CRC64;

Query Match 93.8%; Score 345; DB 1; Length 65;  
 Best Local Similarity 92.3%; Pred. No. 6.6e-31;  
 Matches 60; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
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 AC P28505;  
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 DB 1 VVYDCTESQNLCLCEGSNVCGEGNKCILGSNGERNQCVTGECPKQPSHNDGFEETP 60  
 DR 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-DEC-1992 (Rel. 24, Last annotation update)  
 DE Hirudin II.  
 OS Hirudo medicinalis (Medicinal leech);  
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
 OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.



Query Match	85.6%	Score 315; DB 1; Length 66;	Best Local Similarity 87.1%; Pred. No. 1.e-27;	Indels 0; Gaps 0;	OC Eukaryota; Metzooa; Annelida; Clitellata; Hirudinida; Hirudinea;
Matches	54;	Conservative 4;	Mismatches 4;	Indels 0;	OC Arynchobdella; Hirudiniformes; Hirudinidae; Hirudinaria.
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Db					OX [1]
Qy	61	EE 62			RN RP SEQUENCE.
Db	61	ED 62			RC TISSUE=Head;
RESULT	13				RX MEDLINE=940033; PubMed=8397794;
ITHA_HIRME		STANDARD;	PRT;	65 AA.	RA Electricwala A., Hartwell R., Scawen M.D., Atkinson T.;
ID	ITHA_HIRME				RT "The complete amino acid sequence of a hirudin variant from the leech
AC	P28501;				RT Hirudinaria manillensis";
DT	01-DEC-1992 (Rel. 24, Last sequence update)				J. Protein Chem. 12:365-370(1993).
DT	16-OCT-2001 (Rel. 40, Last annotation update)				- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
DE	Hirudin I (Fragments)				- INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
OS	Hirudo medicinalis (Medicinal leech).				- THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
OC	Eukaryota; Metzooa; Annelida; Clitellata; Hirudinida; Hirudinea;				-! SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
OC	Arynchobdella; Hirudiniformes; Hirudinidae; Hirudo.				DR HSSP; P01050; SHIR.
OX	NCBI-TaxID=6421;				DR InterPro; IPR00429; Hirudin.
RN	{1}				DR Pfam; PF00713; Hirudin; 1.
RP	SEQUENCE;				DR PRINTS; PR00777; HIRUDIN.
RX	MEDLINE=90005945; PubMed=2792365;				DR PRODOM; P004216; Hirudin; 1.
RA	Scharr M., Engels J., Trippel D.;				DR Serine protease inhibitor; Multigene family.
RT	"Primary structures of new iso-hirudins".;				FT DR DISURPID 6 14 BY SIMILARITY.
RL	FEBs Lett. 25:105-110(1989)				FT FT DISURPID 16 28 BY SIMILARITY.
CC	- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE				FT FT DISURPID 22 37 BY SIMILARITY.
CC	INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-				FT SQ SEQUENCE 63 AA; 6699 MW; 8BC2B2B85C51BED CRC64;
CC	THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.				
-i SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.					
DR					
DR	HSSP; P01050; IHAG.				
DR	InterPro; IPR00429; Hirudin.				
DR	Pfam; PF00713; Hirudin; 1.				
PRINTS; PR00777; HIRUDIN					
DR	PRODOM; P004216; Hirudin; 1.				
DR	Serine protease inhibitor; Multigene family.				
FT	disurpid 6 14 BY SIMILARITY.				
FT	disurpid 16 28 BY SIMILARITY.				
FT	disurpid 22 37 BY SIMILARITY.				
FT	MOD RES 63 SULFATION .				
SQ	SEQUENCE 65 AA; 7126 MW; B79C5A9D1677ADS CRC64;				
RESULT	15				
ITH6_HIRMA		STANDARD;	PRT;	63 AA.	
ID	ITH6_HIRMA				
AC	P28512;				
DT	01-DEC-1992 (Rel. 24, Created)				
DT	01-DEC-1992 (Rel. 24, Last sequence update)				
DB	1 VSYTDCTESGONLCLCEGSNVCGKGNKCTIGSDGERKNQCVTGEGTPKPOSHNDGFEEIP 58				
Qy	61 ERYLQ 65				
Db	59 DEXIK 63				
RESULT	15				
ITH6_HIRMA		STANDARD;	PRT;	63 AA.	
ID	ITH6_HIRMA				
AC	P28512;				
DT	01-DEC-1992 (Rel. 24, Created)				
DT	01-DEC-1992 (Rel. 24, Last sequence update)				
DB	1 VSYTDCTESGONLCLCEGSNVCGKGNKCTIGSDGERKNQCVTGEGTPKPOSHNDGFEEIP 58				
Qy	61 ERYLQ 65				
Db	59 DEXIK 63				
RESULT	15				
ITH6_HIRMA		STANDARD;	PRT;	63 AA.	
ID	ITH6_HIRMA				
AC	P28512;				
DT	01-DEC-1992 (Rel. 24, Created)				
DT	01-DEC-1992 (Rel. 24, Last sequence update)				
DB	1 VSYTDCTESGONLCLCEGSNVCGKGNKCTIGSDGERKNQCVTGEGTPKPOSHNDGFEEIP 58				
Qy	61 ERYLQ 65				
Db	59 DEXIK 63				
RESULT	14				
ITHV_HIRMA		STANDARD;	PRT;	63 AA.	
ID	ITHV_HIRMA				
AC	P81497;				
DT	15-DEC-1998 (Rel. 37, Created)				
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DT	15-DEC-1998 (Rel. 37, Last annotation update)				
DE	Hirudin RIVI (Buftrudin).				
OS	Hirudinaria manillensis (Buffalo leech).				
KW	Hirudinaria manillensis (Buftrudin).				
RESULT	14				
ITHV_HIRMA		STANDARD;	PRT;	63 AA.	
ID	ITHV_HIRMA				
AC	P81497;				
DT	15-DEC-1998 (Rel. 37, Created)				
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DT	15-DEC-1998 (Rel. 37, Last annotation update)				
DE	Hirudin RIVI (Buftrudin).				
OS	Hirudinaria manillensis (Buffalo leech).				



